

### In The Specification:

Please enter the paper copy of the Sequence Listing into the Specification.

*On page 4, please amend the paragraph beginning on line 8 and ending on line 26 as follows:*

Figure 1 shows the sequence alignment of the 16S rRNA sequence of *Marinomonas protea* (SEQ ID No 1) (Figure 3) to the corresponding sequence of *Marinomonas communis* (SEQ ID No 4);

Figure 2 is a phylogenetic tree comparing *Marinomonas protea* with its closest phylogenetic relatives.

Figure 3 shows the 16S rRNA sequence alignment of isolate 20 (seq ID 2, upper case) to *Marinomonas protea* 16S rRNA (Seq ID 1; lower case) showing 89.4% similarity.

Figure 4 shows the 16S rRNA sequence alignment of isolate 20 (seq ID 2) to its closest phylogenetic relative *Pseudomonas synxantha* (SEQ ID No 5) showing 99.4% similarity.

Figure 5 is a phylogenetic tree based on 16S rRNA sequences comparing Isolate 20 (SEQ ID 2) with its closest relatives. Multiple sequence alignments were created using the Clustal method with a gap penalty of 10.

Figure 6 shows the result of an RI experiment at time= 0 (6A) and at time = 60 minutes (6B).

Figure 7, 8, 9 relate to the Vickers hardness test as described in the example.